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Application No: 10549506   Version No: 2.0

Input Set:

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<110>   Bayer HealthCare LLC

        Haaning, Jesper Mortensen

        Andersen, Kim Vilbour

        Ropke, Mads

        Glazer, Steven

<120>   FVII or FVIIa Variants

<130>   0272wo310

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<141>   2006-07-07

<150>   US 60/456,547

<151>   2003-03-20

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aat gcc ttt ctg gaa gag ctc cgc cct ggc tcc ctg gaa cgc gaa tgc   165
Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys
         5   10   15

aaa gag gaa cag tgc agc ttt gag gaa gcc cgg gag att ttc aaa gac   213
Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys Asp
        20   25   30

gct gag cgg acc aaa ctg ttt tgg att agc tat agc gat ggc gat cag   261
Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln
    35   40   45

tgc gcc tcc agc cct tgc cag aac ggg ggc tcc tgc aaa gac cag ctg   309
Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu
50   55   60   65

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cag agc tat atc tgc ttc tgc ctg cct gcc ttt gag ggg cgc aat tgc       357
Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn Cys
                70              75                  80

gaa acc cat aag gat gac cag ctg att tgc gtc aac gaa aac ggg ggc       405
Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly Gly
                85              90                  95

tgc gag cag tac tgc agc gat cac acg ggc acg aag cgg agc tgc cgc       453
Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys Arg
            100             105             110

tgc cac gaa ggc tat agc ctc ctg gct gac ggg gtg tcc tgc acg ccc       501
Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro
        115             120             125

acg gtg gaa tac cct tgc ggg aag att ccc att cta gaa aag cgg aac       549
Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn
130             135             140             145

gct agc aaa ccc cag ggc cgg atc gtc ggc ggg aag gtc tgc cct aag       597
Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro Lys
                150             155             160

ggg gag tgc ccc tgg cag gtc ctg ctc ctg gtc aac ggg gcc cag ctg       645
Gly Glu Cys Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala Gln Leu
            165             170             175

tgc ggc ggg acc ctc atc aat acc att tgg gtc gtg tcc gcc gct cac       693
Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala His
        180             185             190

tgc ttc gat aag att aag aat tgg cgg aac ctc atc gct gtg ctc ggc       741
Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu Gly
        195             200             205

gaa cac gat ctg tcc gag cat gac ggg gac gaa cag tcc cgc cgg gtg       789
Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg Val
210             215             220             225

gct cag gtc atc att ccc tcc acc tat gtg cct ggc acg acc aat cac       837
Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His
                230             235             240

gat atc gct ctg ctc cgc ctc cac cag ccc gtc gtg ctc acc gat cac       885
Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp His
        245             250             255

gtc gtg cct ctg tgc ctg cct gag cgg acc ttt agc gaa cgc acg ctg       933
Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr Leu
        260             265             270

gct ttc gtc cgc ttt agc ctc gtg tcc ggc tgg ggc cag ctg ctc gac       981
Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu Asp
        275             280             285
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cgg ggc gct acc gct ctc gag ctg atg gtg ctc aac gtc ccc cgg ctg      1029
Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg Leu
290             295             300             305

atg acc cag gac tgc ctg cag cag tcc cgc aaa gtg ggg gac tcc ccc      1077
Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser Pro
                310             315             320

aat atc acg gag tat atg ttt tgc gct ggc tat agc gat ggc tcc aag      1125
Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser Lys
            325             330             335

gat agc tgc aag ggg gac tcc ggc ggg ccc cat gcc acg cac tat cgc      1173
Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr Arg
            340             345             350

ggg acc tgg tac ctc acc ggg atc gtc agc tgg ggc cag ggc tgc gcc      1221
Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys Ala
        355             360             365

acg gtg ggg cac ttt ggc gtc tac acg cgc gtc agc cag tac att gag      1269
Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu
370             375             380             385

tgg ctg cag aag ctc atg cgg agc gaa ccc cgg ccc ggg gtg ctc ctg      1317
Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu Leu
            390             395             400

cgg gcc cct ttc cct tga taa                                          1338
Arg Ala Pro Phe Pro
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<213>   Homo sapiens

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Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu
1               5               10              15


Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys
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Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp
        35              40              45


Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln
        50              55              60


Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn
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Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly
                    85   90   95

Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys
                    100   105   110

Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr
                    115   120   125

Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg
        130   135   140

Asn Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro
145   150   155   160

Lys Gly Glu Cys Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala Gln
                    165   170   175

Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala
                    180   185   190

His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu
        195   200   205

Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg
        210   215   220

Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn
225   230   235   240

His Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp
                    245   250   255

His Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr
                    260   265   270

Leu Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu
                    275   280   285

Asp Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg
        290   295   300

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Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser
305                 310                 315                 320


Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser
                325                 330                 335


Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr
            340                 345                 350


Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys
        355                 360                 365


Ala Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile
    370                 375                 380


Glu Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu
385                 390                 395                 400


Leu Arg Ala Pro Phe Pro
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<213>   Artificial

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<223>   Synthetic gene for optimized expression of hFVII

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gcgccgggcc aatgcctttc tggaagagct ccgccctggc tccctggaac gcgaatgcaa       180

agaggaacag tgcagctttg aggaagcccg ggagatttttc aaagacgctg agcggaccaa       240

actgttttgg attagctata gcgatggcga tcagtgcgcc tccagccctt gccagaacgg       300

gggctcctgc aaagaccagc tgcagagcta tatctgcttc tgcctgcctg cctttgaggg       360

gcgcaattgc gaaacccata aggatgacca gctgatttgc gtcaacgaaa acggggggctg       420

cgagcagtac tgcagcgatc acacgggcac gaagcggagc tgccgctgcc acgaaggcta       480

tagcctcctg gctgacgggg tgtcctgcac gcccacggtg gaataccctt gcgggaagat       540
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tcccattcta gaaaagcgga acgctagcaa accccagggc cggatcgtcg gcgggaaggt          600

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cggcgggacc ctcatcaata ccatttgggt cgtgtccgcc gctcactgct tcgataagat          720

taagaattgg cggaacctca tcgctgtgct cggcgaacac gatctgtccg agcatgacgg          780

ggacgaacag tcccgccggg tggctcaggt catcattccc tccacctatg tgcctggcac          840

gaccaatcac gatatcgctc tgctccgcct ccaccagccc gtcgtgctca ccgatcacgt          900

cgtgcctctg tgcctgcctg agcggacctt tagcgaacgc acgctggctt tcgtccgctt          960

tagcctcgtg tccggctggg gccagctgct cgaccggggc gctaccgctc tcgagctgat         1020

ggtgctcaac gtcccccggc tgatgaccca ggactgcctg cagcagtccc gcaaagtggg         1080

ggactccccc aatatcacgg agtatatgtt ttgcgctggc tatagcgatg gctccaagga         1140

tagctgcaag ggggactccg gcgggcccca tgccacgcac tatcgcggga cctggtacct         1200

caccgggatc gtcagctggg gccagggctg cgccacggtg gggcactttg gcgtctacac         1260

gcgcgtcagc cagtacattg agtggctgca gaagctcatg cggagcgaac cccggcccgg         1320

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<212>   DNA
<213>   Artificial
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cccattctag aaaagcggaa cgccagcaaa ccccaggg   38

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<220>
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cgccgctcac tgcttcaaca agattaagaa ttgg   34

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<220>
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<210> 11

<211> 22
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<220>
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